AMENDMENTS TO THE SPECIFICATION

Please delete the existing sequence listing and insert the accompany Sequence Listing (pages 1-111).

Amend the paragraph at page 44, lines 4-11 as follows:

When it is desired to link the indicator to a solid support through the peptide backbone, the peptide backbone may comprise an additional peptide spacer (designated S^1 or S^2 in Formula I). The spacer may be present at either the amino or carboxyl terminus of the peptide backbone and may vary from about 1 to about 50 amino acids, more preferably from 1 to about 20 and most preferably from 1 to about 10 amino acids in length. Particularly preferred spacers include Asp-Gly-Ser-Gly-Gly-Gly-Glu-Asp-Glu-Lys (SEQ ID NO:243—), Lys-Glu-Asp-Gly-Gly-Asp-Lys (SEQ ID NO:244—), Asp-Gly-Ser-Gly-Glu-Asp-Glu-Lys (SEQ ID NO:245—), and Lys-Glu-Asp-Glu-Gly-Ser-Gly-Asp-Lys (SEQ ID NO:246—).

Amend the paragraph at page 67, lines 27-31, as follows:

For apoptosis-related protease activity determination, 10 μM concentration of the compounds listed in Example ~~8~~ 7 (compound structures 2 through 13) were incubated with cells for 30 min. to 3 hours. The cells were then washed similarly twice. Using glass capillary tubes, the washed cells were transferred and examined under a fluorescence microscope.

Amend the paragraph at page 15, line 17, through page 16, line 7, as follows:

Figure 5 illustrates fluorescence of a DEVD, a DEVN, and an ICE substrate. To one hundred μl of assay buffer (50mM HEPES buffer pH 7.5, 10% (w/v) sucrose and 0.1% (w/v) CHAPS) containing 1μM of a DEVD substrate ~~DEVD (compound 2 of Example 8)~~, a DEVN substrate, ~~DEVN (compound 3 of Example 8)~~ and an ICE substrate ~~(compound 5 of Example 8)~~ 10μl of Jurkat cell lysate was added and incubated for 16 hours at 37°C. The Jurkat cells' lysate was prepared from the cells that had been stimulated by antiFas antibody at 1μg/ml concentration for 6 hours. The fluorescence intensity for the substrate solution alone is indicated in Figure 5 as a horizontal lined bar marked as t = 0 hr and the fluorescence intensity of the lysate and substrate solution mixture after 16 hr

is indicated by vertical line bar and is marked as t = 16 hr digestion. 10 µl cell lysate was pre-incubated with 50 µm ZVAD-FMK (benzyoxycarbonyl valanyl alanyl aspartyl-fluoromethylketone) at 37°C for 30 min. then added to the substrate solution. The fluorescence intensity after 16 hours for this mixture is indicated by the bar marked as ZVAD-FMK (inhibitor). Lastly, pre-incubated cell lysate with iodoacetamide(alkylating agent for sulfhydryl group) and PMSF (for inhibiting serine proteases) was added to the substrate solution. The fluorescence intensity after 16 hours at 37°C is indicated by bar marked as Iodoacetamide/PMSF. The DEVN substrate is a negative control substrate where the P1, Asp, residue is replaced by Asn. The CPP32 protease requires the P1 residue to be aspartic acid residue. The four bar graphs for the DEVN substrate (Fig. 5) clearly indicate that the activated cell lysate do not contain any other protease that digest the DEVD substrate, since the intensity for 16 hour digestion is the same as the substrate alone. The bar graphs for the DEVD substrate indicate that the activate cell lysate do contain CPP32 protease and this protease activities are inhibited by ZVAD-FMK, known CPP32 protease inhibitor. The contribution of any other proteases in digesting DEVD substrate is very small as indicated by the difference between the intensities of ZVAD-FMK bar to Iodoacetamide/PMSF bar.

Amend the paragraph at page 63, lines 8-11, as follows:

Fluorophores were linked to the amino terminus via the α-amino group of Aspartic acid residue (D) and to the ε-amino group of lysine (K). Labeling was accomplished by the displacement of a succinimidyl group linked to 6-TMR or DER. The structure of the peptide, called ~~NorFES-KGY~~ NorFES is:

Amend the paragraph at page 64, lines 3-13 as follows:

The observation of the ground-state dimer for the compounds synthesized according to the present invention predicted a significant level of fluorescent quenching for doubly-labeled peptide with the same fluorophore as those compounds listed in Table 11. In fact this prediction was confirmed; a comparison of ~~6-TMR-NorFES-KGY-DER~~ 6-TMR-NorFES-DER with 6-~~TMR-NorFES-KGY-6-TMR~~ TMR-NorFES-6-TMR, *i.e.*, the hetero doubly-labeled with the homo doubly-labeled peptides, indicates the degree of quenching is slightly higher in the hetero- vs. the homo- (94 vs. 90%). The fluorescein derivative, however, exhibited only 55% quenching. The

symbols I_0 and I_c for the percent fluorescent quenching (%Q) refer to the fluorescence intensity for the intact labeled peptide and the enzyme digested labeled peptide solution respectively.

Amend the paragraphs at page 64, line 19 through page 65, line 9 as follows:

The substrate sequence could be extended by one amino acid residue and the fluorophore could be attached through the episilon amino group on the lysine residue's side chain without major perturbation to the amount of observed quenching. Specifically, this addition (peptides designated ~~K-NorFES-KGY~~ K-NorFES) resulted in a slight decrease in cleavability rate and a very slight increase in the percent quenching for both the hetero- and homo-doubly-labeled peptide (in the ~~K-NorFES-KGY~~ K-NorFES peptides, N-terminal labeling was via the epsilon-amino group of lysine rather than the α-amino terminus).

Rates of cleavage ($T_{1/2}$) of these substrates by elastase were also measured by recording the time after addition of the protease at which the signal was one-half maximum (*see*, Table 11). a comparison of three homo-doubly-labeled peptides, *i.e.*, ~~NorFES-KGY~~ NorFES labeled with two molecules of 6-TMR, DER, and fluorescein (Fl), shows the order of cleavability to be: ~~Fl-NorFES-KGY-Fl > 6-TMR-NorFES-KGY-6-TMR > DER-NorFES-KGY-DER~~ Fl-NorFES-Fl > 6-TMR-NorFES-6-TMR > DER-NorFES-DER.